

PARAMVIR DEHAL

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EDUCATION

Ph.D.	University of California, Davis	Genetics	2003
B.S.	University of California, Davis	Genetics	1998

RESEARCH EXPERIENCE

- 9/03-current **Postdoctoral Fellow, Computer Science**
Joint Genome Institute, Evolutionary Genomics Dept.
- Demonstrated that two rounds of whole genome duplication occurred in the ancestral vertebrate
 - Created the Phylogenetically Inferred Groups (PhIGs) database, a resource for phylogenomic gene family clustering and automated creation of gene trees for eukaryotic and prokaryotic genomes (<http://phigs.org>)
 - Performed comparative and evolutionary analysis for the *Phytophthora sojae* and *Phytophthora ramorum* genome projects
 - Determine species relationship of sequenced bacteria and eukaryotes by creating phylogenetic trees from concatenated single copy genes
- 6/99-8/03 **Graduate Student Researcher**
Lawrence Berkeley & Lawrence Livermore National Labs
- Led comparative and sequence analysis for the *Ciona intestinalis* genome project
 - Led development of the JGI genome portal and genome annotation pipeline, including writing programs, database schemas, computational infrastructure, compute cluster job scheduler and key concepts for JGI genome annotation
 - Comparative analysis of Human Chromosome 19 and the related regions in mouse
 - Sequence analysis for the *Takifugu rubripes*, Diatom and Lactic Acid Bacteria genome projects including gene prediction, automated annotation and comparative analysis for publication
- 6/95-6/98 **Undergraduate Student Researcher**
UC Davis
- Performed standard molecular genetics laboratory techniques including, DNA isolation, PCR, RFLPs, AFLPs, cloning, sequencing prep
 - Linkage analysis and QTL identification

PUBLICATIONS

Dehal, P., and J.L. Boore. 2005. Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate. *PLoS Biol* 3: e314.

Dehal, P., and J. L. Boore. 2005. A Phylogenomic Gene Cluster Resource: The Phylogenetically Inferred Groups (PhIGs) Database. *BMC Bioinformatics* in press.

Dehal, P., et al. 2002. The draft genome of *Ciona intestinalis*: insights into chordate and vertebrate origins. *Science* 298: 2157-2167.

Dehal, P., P. Predki, A.S. Olsen, A. Kobayashi, P. Folta, S. Lucas, M. Land, A. Terry, C.L. Ecale Zhou, S. Rash, Q. Zhang, L. Gordon, J. Kim, C. Elkin, M.J. Pollard, P. Richardson, D. Rokhsar, E. Uberbacher, T. Hawkins, E. Branscomb, and L. Stubbs. 2001. Human chromosome 19 and related regions in mouse: conservative and lineage-specific evolution. *Science* 293: 104-111.

Li, H., A. Coghlan, J. Ruan, L. J. Coin, J.-K. Heriche, R. Li, Z. Zhang, L. Boulnd, W. Zheng, **P. Dehal**, J. Wang, and R. Durbin. 2005. TreeFam: a curated database of phylogenetic trees of animal gene families. *Nucleic Acids Research* submitted.

Grimwood, J., et al. including **P. Dehal**. 2004. The DNA sequence and biology of human chromosome 19. *Nature* 428: 529-535.

Saunders, N.F., et al. including **P. Dehal**. 2003. Mechanisms of thermal adaptation revealed from the genomes of the Antarctic Archaea *Methanogenium frigidum* and *Methanococcoides burtonii*. *Genome Res* 13: 1580-1588.

Aparicio, S., et al. including **P. Dehal**. 2002. Whole-genome shotgun assembly and analysis of the genome of *Fugu rubripes*. *Science* 297: 1301-1310.

Kim, J., L. Gordon, **P. Dehal**, H. Badri, M. Christensen, M. Groza, C. Ha, S. Hammond, M. Vargas, E. Wehri, M. Wagner, A. Olsen, and L. Stubbs. 2001. Homology-driven assembly of a sequence-ready mouse BAC contig map spanning regions related to the 46-Mb gene-rich euchromatic segments of human chromosome 19. *Genomics* 74: 129-141.

Meeting Abstracts

Dehal, P. and L. Stubbs, 2001 Human chromosome 19 and related regions in mouse: conservative and lineage-specific evolution. Biology of Genomes, Cold Spring Harbor Lab, NY.

Dehal, P., and J. L. Boore, 2003 Dynamics of Gene Duplication Revealed by Comparing Complete Genomes of a Tunicate, Fish, Mouse, and Man. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA (contributed talk).

Dehal, P., and J. L. Boore, 2004 Mode and Tempo of Gene Duplication in the Ancestral Vertebrate. Biology of Genomes, Cold Spring Harbor Laboratory, NY (poster presentation).

Dehal, P., and J. L. Boore, 2004 Insights Into the Evolution of Gene Structure Using Whole Genome Sequences. Annual meeting of the Society for Molecular Biology and Evolution, Pennsylvania State University, PA (poster presentation).

Dehal, P., and J. L. Boore, 2004 Two Round of Genome Duplication in the Ancestral Vertebrate. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO (contributed talk).

Dehal, P., and J. L. Boore, 2004 PhIGs: Phylogenetically Inferred Groups, a Resource for Comparative Genomics. Genome Informatics, Sanger Centre, Hinxton, UK (contributed talk).

Dehal, P., and J. L. Boore, 2005 PhIGs: A Tool for Whole Genome Evolutionary Analysis. Annual meeting of the Society for the Study of Evolution, Fairbanks, Alaska (poster presentation).

Dehal, P., and J. L. Boore, 2005 PhIGs: A Tool for Whole Genome Evolutionary Analysis. Biology of Genomes, Cold Spring Harbor Laboratory, NY (poster presentation).

Dehal, P., and J. L. Boore, 2005 Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate. Biology of Genomes, Cold Spring Harbor Laboratory, CSHL, NY (poster presentation).

Dehal, P., and J. L. Boore, 2005 Timing the Vertebrate Genome Duplications. Genome Informatics, Cold Spring Harbor Laboratory, CSHL, NY (contributed talk).